RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/732,597   TIME: 10:15:55

Input Set : A:\BB1413 US NA Seq Listing.txt
Output Set: N:\CRF3\12212000\I732597.raw

ENTERED

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     2 <110> APPLICANT: Cahoon, Edgar B.
     3        Cahoon, Rebecca E.
     5 <120> TITLE OF INVENTION: Enzymes Involved In Petroselinic Acid Biosynthesis
     7 <130> FILE REFERENCE: BB1413 US NA
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/732,597
C--> 10 <141> CURRENT FILING DATE: 2000-12-08
    12 <150> PRIOR APPLICATION NUMBER: 60/169,968
W--> 13 <151> PRIOR FILING DATE: 9 DECEMBER 1999
    15 <160> NUMBER OF SEQ ID NOS: 12
    17 <170> SOFTWARE: Microsoft Office 97
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 1344
    21 <212> TYPE: DNA
    22 <213> ORGANISM: Hedera helix
    24 <220> FEATURE:
    25 <221> NAME/KEY: unsure
    26 <222> LOCATION: (997)
    28 <400> SEQUENCE: 1
    29 caaccccaga aaataaaaat aaaaactcaa gaagaagaag aagaaatggc tttgaagctc   60
    30 aatttccaat gcaagaagaa ccaccctgct gcgtttgcta agtcaccatt accagtgacc  120
    31 agagttagct ctccaagggt tttcatggct tccactgtca actctaactc catggttctt  180
    32 gataatctca aaagtccgcc aaatcttcaa gtcactcact ctatgccacc ccaaaagcta  240
    33 gaaatattca agtcccttga tgattgggct aggaacaatg tgttgattca cctcaaatct  300
    34 gtcgagaaat cttggcaacc acaagactac ttgccggatc cggtgtcaga cggattcgag  360
    35 gagcaagtgc gggagttgag ggaaagggcc aaggagattc ccgacgacta tttttgtggtg  420
    36 ttagttggag atatgatcac agaagaagca cttccaacat atatgtctat gctcaatagg  480
    37 tgtgatggta ttaaggatga gactggggct gagcccagtg cttgggcaat gtggactagg  540
    38 gcatggactg ccgaagagaa tagacatggt gaccttctca ataagtacct ttatttgtct  600
    39 ggaagggttg atatgaggaa aattgagaag actattcaat atctcatcgg ctcaggaatg  660
    40 gatatcaagt cagaaaacag cccctaccta ggcttcatct acacatcctt ccaagagaga  720
    41 gcaaccttca tatcccatgc caacacagcc aagctggccc aacactacgg cgacaagaac  780
    42 ctcgctcaca tctgcggctc catcgcctcc gacgacgaagc gccacgccac agcctacacc  840
    43 aagatcgtgg aaaagctcgc tgagatcgac cccgacacaa cagtaattgc ttttgcagat  900
    44 atgatgcgca aaaaataac aatgccagcg cacttgatgt acgacggaag tgacgaactt  960
W--> 45 ctttttaaac atttcacggc ggttgctcag agagtgnggg tttattctgc gttggattat 1020
    46 tgcgacatct tagagtttct ggtggataaa tggaatgtgg aaaggcttac ggggctgtcg 1080
    47 gacgagggggc gaaaagcgca ggaatatgtg tgtgaattgg gtcccaagat taggcgagtg 1140
    48 gaagagaaag tgcagggggaa ggagaagaag aagaaagctg agcaccctgt ttctttcagc 1200
    49 tggattttca atcgggagtt gaagatatga acaggaaggg aagggaatgg aggagcaaat 1260
    50 gagtgtagta gatttctata tgcatgttta tatattatga atgattatta tataataata 1320
    51 agtgttttgag ttttaagtaa aaaa                                          1344
    53 <210> SEQ ID NO: 2
    54 <211> LENGTH: 394
    55 <212> TYPE: PRT
    56 <213> ORGANISM: Hedera helix
    58 <220> FEATURE:
    59 <221> NAME/KEY: UNSURE
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RAW SEQUENCE LISTING
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TIME: 10:15:55

Input Set : A:\BB1413 US NA Seq Listing.txt
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60 <222> LOCATION: (318)
62 <400> SEQUENCE: 2
63 Met ala Leu Lys Leu Asn Phe Gln Cys Lys Lys Asn His Pro Ala Ala
64   1               5                   10                  15
66 Phe Ala Lys Ser Pro Leu Pro Val Thr Arg Val Ser Ser Pro Arg Val
67              20                  25                  30
69 Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
70          35                  40                  45
72 Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
73          50                  55                  60
75 Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
76   65                  70                  75                  80
78 Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
79              85                  90                  95
81 Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
82              100                 105                 110
84 Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
85          115                 120                 125
87 Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
88          130                 135                 140
90 Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
91 145                 150                 155                 160
93 Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
94              165                 170                 175
96 Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
97              180                 185                 190
99 Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
100             195                 200                 205
102 Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
103         210                 215                 220
105 Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
106 225                 230                 235                 240
108 Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
109             245                 250                 255
111 Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
112             260                 265                 270
114 Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
115         275                 280                 285
117 Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
118         290                 295                 300
```
W-->
```
120 Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr
121 305                 310                 315                 320
123 Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
124             325                 330                 335
126 Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
127             340                 345                 350
129 Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
130         355                 360                 365
132 Val Gln Gly Lys Glu Lys Lys Lys Ala Glu His Pro Val Ser Phe
```

```
133      370                    375                    380
135 Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
136 385                    390
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 445
140 <212> TYPE: DNA
141 <213> ORGANISM: Hedera helix
143 <400> SEQUENCE: 3
144 cttcgtgctc tccgcctctt gttttttttct ctttccaaat attttctgag taattttctc  60
145 agatctattc ctctttcttc tctccctaat ttgatccatc aatggcttct gttactgcct 120
146 catcgatttc cttcacctct atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180
147 gttcaatttc actctctgtc aatgggaaat ccttccgttc acttaggttg ctgtcggcac 240
148 cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300
149 ttgtgcggaa acaactggcg ctgccgctga ttctgcaagt cactggagag tcaaaattcg 360
150 cagcgcttgg ggctgattct ctcgacacgg ttgagattgt gatgggacta aaggaggaat 420
151 tcggaatcaa gcgtgggaaa aagaa                                        445
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 114
155 <212> TYPE: PRT
156 <213> ORGANISM: Hedera helix
158 <400> SEQUENCE: 4
159 Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser
160  1                5                   10                   15
162 Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser
163               20                   25                   30
165 Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
166            35                   40                   45
168 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
169      50                   55                   60
171 Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val
172 65                   70                   75                   80
174 Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
175               85                   90                   95
177 Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly
178            100                  105                  110
180 Lys Lys
181    114
183 <210> SEQ ID NO: 5
184 <211> LENGTH: 920
185 <212> TYPE: DNA
186 <213> ORGANISM: Hedera helix
188 <400> SEQUENCE: 5
189 cttcgtgctc tccgcctctt gttttttttct ctttccaaat attttctgag taattttctc  60
190 agatctattc ctctttcttc tctccctaat ttgatccatc aatggcttct gttactgcct 120
191 catcgatttc cttcacctct atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180
192 gttcaatttc actctctgtc aatgggaaat ccttccgttc acttaggttg ctgtcggcac 240
193 cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300
194 ttgtgcggaa acaactggcg ctgccgctg attctgcagt cactggagag tcaaaattcg 360
195 cagcgcttgg ggctgattct ctcgacacgg ttgagattgt gatgggacta gaggaggaat 420
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PATENT APPLICATION: US/09/732,597   TIME: 10:15:55

Input Set : A:\BB1413 US NA Seq Listing.txt
Output Set: N:\CRF3\12212000\I732597.raw

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196 tcggaatcag cgtggaagaa gaaagtgcac agaccattgc cactgttcaa gatgcagcgg 480
197 acctgattga gaagcttgtt gagaaaaagg agtagaagaa ccggggtaga aattctgcaa 540
198 aataggttta ttaaggacag ttactttatt aggatggttc atcaagatct tcattaccct 600
199 acatttattt gtatgctcct catgaagccg caaaagtagt agtggtgatg aaatttaccc 660
200 cgagtcttcg ccttaattat caaagtgaga gagccagaaa aagaggctat gctatctctc 720
201 atctcgttat gttttatttt cttgtcggac ttctggttgg agttttttt ttttatctaa 780
202 acatgatatt agtcttgttt aaaagtttct caaaaaaata tatcttgttg ttgagactga 840
203 tggagttatt gctcttgata ttttgaatgt attttgagtt attcaaaaaa aaaaaaaaaa 900
204 aaaaaaaaa aaaaaaaaaa                                             920
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 137
209 <212> TYPE: PRT
210 <213> ORGANISM: Hedera helix
212 <400> SEQUENCE: 6
213 Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser
214  1               5                  10                  15
216 Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser
217              20                  25                  30
219 Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
220          35                  40                  45
222 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
223      50                  55                  60
225 Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val
226  65                  70                  75                  80
228 Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
229              85                  90                  95
231 Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu
232          100                 105                 110
234 Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gln Asp Ala Ala Asp Leu
235          115                 120                 125
237 Ile Glu Lys Leu Val Glu Lys Lys Glu
238     130                 135
241 <210> SEQ ID NO: 7
242 <211> LENGTH: 385
243 <212> TYPE: PRT
244 <213> ORGANISM: Coriandrum sativum
246 <400> SEQUENCE: 7
247 Met Ala Met Lys Leu Asn Ala Leu Met Thr Leu Gln Cys Pro Lys Arg
248  1               5                  10                  15
250 Asn Met Phe Thr Arg Ile Ala Pro Pro Gln Ala Gly Arg Val Arg Ser
251              20                  25                  30
253 Lys Val Ser Met Ala Ser Thr Leu His Ala Ser Pro Leu Val Phe Asp
254          35                  40                  45
256 Lys Leu Lys Ala Gly Arg Pro Glu Val Asp Glu Leu Phe Asn Ser Leu
257      50                  55                  60
259 Glu Gly Trp Ala Arg Asp Asn Ile Leu Val His Leu Lys Ser Val Glu
260  65                  70                  75                  80
262 Asn Ser Trp Gln Pro Gln Asp Tyr Leu Pro Asp Pro Thr Ser Asp Ala
263              85                  90                  95
```

```
265 Phe Glu Asp Gln Val Lys Glu Met Arg Glu Arg Ala Lys Asp Ile Pro
266         100                 105             110
268 Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala
269         115                 120             125
271 Leu Pro Thr Tyr Met Ser Met Leu Asn Arg Cys Asp Gly Ile Lys Asp
272     130                 135             140
274 Asp Thr Gly Ala Gln Pro Thr Ser Trp Ala Thr Trp Thr Arg Ala Trp
275 145             150             155             160
277 Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr
278             165                 170             175
280 Leu Ser Gly Arg Val Asp Met Arg Met Ile Glu Lys Thr Ile Gln Tyr
281         180                 185             190
283 Leu Ile Gly Ser Gly Met Asp Thr Lys Thr Glu Asn Cys Pro Tyr Met
284     195                 200             205
286 Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
287     210                 215             220
289 Ala Asn Thr Ala Lys Leu Ala Gln His Tyr Gly Asp Lys Asn Leu Ala
290 225             230             235             240
292 Gln Val Cys Gly Asn Ile Ala Ser Asp Glu Lys Arg His Ala Thr Ala
293             245             250             255
295 Tyr Thr Lys Ile Val Glu Lys Leu Ala Glu Ile Asp Pro Asp Thr Thr
296         260                 265             270
298 Val Ile Ala Phe Ser Asp Met Met Arg Lys Lys Ile Gln Met Pro Ala
299         275                 280             285
301 His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr
302     290                 295             300
304 Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp
305 305             310             315             320
307 Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly
308         325                 330             335
310 Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala
311         340                 345             350
313 Ala Lys Ile Arg Arg Val Glu Gln Lys Val Gln Gly Lys Glu Lys Lys
314     355                 360             365
316 Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile
317     370                 375             380
319 Ile
320 385
322 <210> SEQ ID NO: 8
323 <211> LENGTH: 137
324 <212> TYPE: PRT
325 <213> ORGANISM: Coriandrum sativum
327 <400> SEQUENCE: 8
328 Met Ala Ala Phe Thr Ala Ser Ser Val Ser Phe Thr Pro Leu Ser Ile
329 1             5                 10              15
331 Ser Leu Asn Gln Thr Lys Gly Phe Ala Arg Gly Ser Val Ser Ile Pro
332             20              25              30
334 Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu
335         35              40              45
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/732,597

DATE: 12/21/2000
TIME: 10:15:57

Input Set : A:\BB1413 US NA Seq Listing.txt
Output Set: N:\CRF3\12212000\I732597.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:45 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:45 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:120 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:120 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2